AMENDMENTS TO THE CLAIMS:

Claims 1, 31, and 32 have been amended. The following is the status of the claims of th above-captioned application.

1. (Currently amended) A method of screening a library of polynucleotide sequences of interest having or encoding a desired activity or function ~~characteristic~~ in filamentous fungal cells, wherein the method comprises:

(a) transforming the fungal cells with a population of DNA vectors, wherein each vector comprises:

(i) a fungal selection marker polynucleotide sequence and a fungal replication initiating polynucleotide sequence, wherein the marker and the replication initiating sequence do not vary within the population; and wherein the replication initiating sequence is a nucleic acid sequence selected from the group consisting of: (1) a replication initiating sequence having at least 80% identity with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, as determined using the GAP computer program with a GAP creation penalty of 5.0 and GAP extension penalty of 0.3, and is capable of initiating replication; and (2) replication initiating sequence which hybridises under low stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, or (ii) the respective complementary strands, wherein the low stringency conditions are defined by prehybridization and hybridization at 42°C in 5x SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 25% formamide, and wash conditions are defined at 50°C for 30 minutes in 2x SSC, 0.2% SDS; and

(ii) a polynucleotide sequence of interest, wherein there are vectors in the population that vary from other vectors in the population by carrying different versions of the polynucleotide sequence of interest;

(b) cultivating the cells in the presence of an effective amount of a selective agent or the absence of an appropriate selective agent;

(c) selecting or screening for one or more transformants expressing the desired activity or function ~~characteristic~~; and

(d) isolating the transformant(s) of interest.

2. (Previously presented.) The method according to claim 1, wherein the library of polynucleotide sequences of interest is prepared by random mutagenesis or naturally occurring allelic variations of at least one parent polynucleotide sequence having or encoding a biological activity or function of interest.

3. (Previously presented) The method of claim 1, wherein the polynucleotide sequence further comprises a control sequence.

4. (Previously presented) The method according to claim 1, wherein the polynucleotide sequence of interest encodes a hormone, an enzyme, a receptor or a portion thereof, an antibody or a portion thereof, or a reporter, or a regulatory protein.

5. (Previously presented) The method of claim 4, wherein the enzyme is an oxidoreductase, a transferase, a hydrolase, a lyase, an isomerase, or a ligase.

6. (Previously presented) The method according to claim 4, wherein the enzyme is an aminopeptidase, amylase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase, deoxyribonuclease, esterase, alpha-galactosidase, beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase, invertase, laccase, lipase, mannosidase, mutanase, oxidase, a pectinolytic enzyme, peroxidase, phytase, polyphenoloxidase, a proteolytic enzyme, ribonuclease, transglutaminase, or xylanase.

7. (Previously presented) The method according to claim 3, wherein the control sequence is an enhancer sequence, a leader sequence, a polyadenylation sequence, a propeptide sequence, a promoter, a replication initiation sequence, a signal sequence, a transcriptional terminator or a translational terminator.

8. (Previously presented) The method of claim 7, wherein the promoter is derived from the gene encoding *Aspergillus oryzae* TAKA amylase, NA2-tpi and *Aspergillus niger* or *Aspergillus awamori* glucoamylase.

9. (Previously presented) The method according to claim 1, wherein th selection marker

polynucleotide sequence is selected from the group of genes which encode a product which is responsible for one of th following: resistance to biocid or viral toxicity, resistance to heavy metal toxicity, prototrophy to auxotrophs.

10. (Canceled)

11. (Previously presented) The method of claim 9, wherein the selection marker polynucleotide sequence is a gene selected from the group consisting of *argB* (ornithine carbamoyltransferase), *amdS* (acetamidase), *bar* (phos-hinothricin acetyltransferase), *hemA* (5-aminolevulinate synthase), *hemB* (porphobilinogen synthase), *hygB* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *prn* (proline permease), *pyrG* (orotidine-5'-phosphate decarboxylase), *pyroA*, *riboB*, *sC* (sulfate adenyltransferase), and *trpC* (anthranilate synthase).

12. (Cancelled)

13. (Previously presented) The method of claim 1, wherein the replication initiating polynucleotide sequence has at least 80% identity with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, as determined using the GAP computer program with a GAP creation penalty of 5.0 and GAP extension penalty of 0.3.

14. (Previously presented) The method of claim 1, wherein the replication initiating polynucleotide sequence is obtained from a filamentous fungal cell.

15. (Previously presented) The method of claim 14, wherein the filamentous fungal cell is a strain of *Aspergillus*.

16. (Previously presented) The method of claim 15, wherein the strain of *Aspergillus* is obtained from a strain of *A. nidulans*.

17. (Previously presented) The method of claim 1, wherein the replication initiating polynucleotide sequence has the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:2.

18. (Previously presented) The method of claim 2, wherein the polynucleotide sequence of interest was created by mutagenesis, by random mutagenesis, by use of a physical or chemical mutagenizing agent, by use of a doped oligonucleotide, by DNA shuffling, by subjecting the nucleic acid sequence to PCR generated mutagenesis, or by use of any combination thereof.

19. (Cancelled.)

20. (Previously presented) The method according to claim 1, wherein the filamentous fungal cell transformed with the population of DNA vectors is a cell of a strain of *Acremonium*, *Aspergillus*, *Coprinus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium* or *Trichoderma*.

21. (Previously presented) The method according to claim 20, wherein the cell is an *Aspergillus oryzae*, *Aspergillus niger*, *Aspergillus nidulans*, *Coprinus cinereus*, *Fusarium oxysporum*, or *Trichoderma reesei* cell.

22-29. (Canceled)

30. (Previously presented) The method of claim 1, wherein the polynucleotide sequence of interest is a control sequence.

31. (Currently amended) A method of constructing a library of polynucleotide sequences of interest having or encoding a desired activity or function ~~characteristic~~ in filamentous fungal cells, wherein the method comprises:

(a) transforming the fungal cells with a population of DNA vectors, wherein each vector comprises:

(i) a fungal selection marker polynucleotide sequence and a fungal replication initiating polynucleotide sequence, wherein the marker and the replication initiating sequence do not vary within the population; and wherein the replication initiating sequence is a nucleic acid sequence selected from the group consisting of: (1) a replication initiating sequence having at least 80% identity with the nucl ic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, as determined using the GAP

computer program with a GAP creation penalty of 5.0 and GAP extension penalty of 0.3, and is capable f initiating replication; and (2) replication initiating sequence which hybridises under low stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, or (ii) the respective complementary strands, wherein the low stringency conditions are defined by prehybridization and hybridization at 42°C in 5x SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 25% formamide, and wash conditions are defined at 50°C for 30 minutes in 2x SSC, 0.2% SDS; and

(ii) a polynucleotide sequence of interest having or encoding a desired activity or function ~~characteristic~~, wherein there are vectors in the population that vary from other vectors in the population by carrying different versions of the polynucleotide sequence of interest;

(b) cultivating the cells in the presence of an effective amount of a selective agent or the absence of an appropriate selective agent.

32. (Currently amended) The method of claim 31, further comprising the steps of:

(c) selecting or screening for one or more transformants expressing the desired activity or function ~~characteristic~~; and

(d) isolating the transformant(s) of interest.